

1	1316	33.2	340	11	08C608	08C608	mus musculus
2	707	39.3	159	11	Q9d146	Q9d146	mus musculus
3	358.5	19.9	376	16	08R972	08R972	thermoanaer
4	312	17.3	366	16	08C8D0	08C8D0	staphylococ
5	309.5	17.2	372	16	08E820	08E820	oceanobacill
6	279	15.3	366	16	08NWB9	08NWB9	staphylococ
7	271.5	15.1	258	16	08RE15	08RE15	fusobacteri
8	256	14.2	242	5	08SV52	08SV52	encephallito
9	245	13.6	433	16	08FMR9	08FMR9	corynebacte
10	230	12.8	380	16	08NNG6	08NNG6	corynebacte
11	203.5	11.3	265	16	08DNV4	08DNV4	streptococc
12	203.5	11.3	309	16	08G3M5	08G3M5	bidifidacte
13	189.5	10.5	262	16	08DF99	08DF99	streptococc
14	185.5	10.3	262	2	P95777	P95777	streptococ
15	181.5	10.1	265	2	Q9L462	Q9L462	lactobacill
16	174	9.7	262	16	08DA7	08DA7	streptococc

Db 147 CTTPIHPSRAPDYPTGAGRLEE

ID	Q8C608	PRELIMINARY;	PTI;	340 AA.
AC	Q8C608;			
DT	01-MAR-2003 (Tremblrel. 23, Created)			
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE	Mus musculus (Mouse).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002).			
DR	EMBL; AK076788; BAC36481.1; "			
SQ	SEQUENCE 340 AA; 37822 MW; 82DC63DB90B68B4E CRC64;			
Query Match	73.2%;	Score 1316;	DB 11;	Length 340;
Best Local Similarity	84.6%;	Pred. No. 3.6e-100;		
Matches 253;	Conservative 21;	Mismatches 25;	Indels	0; Gaps 0
1	MDKALLSLINDPASISPAESMDNGLVPESPPTVTMLFLTNDLTREVMEEVLOKKAD	60		
27	MDKALLSLINDPASISPAESMDNGLVPESPPTVTMLFLTNDLTREVMEEVLOKKAD	86		
61	LILSHPIEPIEPRKRIITWNTWKERLVRILENRGVISPHITAYDAAPGVNNMLAKGIG	120		
87	FILSYHPPIEPRKRIITWNTWKERLVRILENRGVISPHITAYDAAPGVNNMLAKGIG	146		
121	CTSRPIHPKAPRYPIEGNHRREFNVNNTQDDKTKMSAVKIGDGVSYTSFARFGNEBOT	180		
147	CTTRPIHPKAPRYPIEGNHRREFNVNNTQDDKTKMSAVKIGDGVSYTSFARFGNEBOT	206		

ID	Query Match	Best Local Similarity	Matches 140;	Conservative 11;	Mismatches 8;	Indels 0;	Gaps 0	Length 159;
QY	181 RINNCQKALMOVAVDVELSRNKKOLYQKTEILSEKPLLIHTGMRCLTIDSVSLAMID	88.1%;	140;	11;	8;	0;	0	159;
Db	207 RINSCQKTLIMQVIAFLSDPRLQYKTEILSEKPLLIHTGMRCLTIDSVSLAMIE							
QY	241 RIKRHLKLSHLRLALGVGRLESQVKKVVALCAGSGSSVLOGVEADLYLTGEMSHHD							
Db	267 RIKRHLKLSHLRLALGVGRLESQVKKVVALCAGSGSSVLOGVEADLYLTGEMSHHD							
RESULT 2								
Q9D146	PRELIMINARY;	PRT;	159 AA.					
Q9D146	AC							
DT	01-JUN-2001 (TREMBlrel. 17, Created)							
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)							
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)							
DE	1110030G24R1k protein.							
GN	1110030G24R1k.							
OS	Mus musculus (Mouse).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.							
OX	NCBI_TaxID=10090;							
RN	(1)							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=C57BL/6J; TISSUE=Embryo;							
RX	MEDLINE=21085660; PubMed=11217851;							
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,							
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi T., Fukuda S.,							
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,							
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,							
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,							
RA	Fleischmann W., Gaasterland T., Glass C., Kling B., Koehli H.,							
RA	Kuehl P., Lewis S., Matsuo Y., Nikiado I., Pesole G., Quackenbush J.,							
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,							
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,							
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,							
RA	Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,							
RA	Gustincich S., Hall D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,							
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,							
RA	Nordone P., Rung B., Ringwald M., Rodriguez I., Sakamoto N.,							
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,							
RA	Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,							
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,							
RA	Hayashizaki Y.;							
RT	*Functional annotation of a full-length mouse cDNA collection.*;							
RL	EMBL: AK003978; BMB23102.1;							
DR	EMBL: AK003978; BMB23102.1;							
DR	MGI: 1913428; 1110030G24R1k.							
DR	InterPro: IPR002678; DUF34.							
DR	Pfam: PF01784; DUF34; 1.							
SO	SEQUENCE 159 AA; 17559 MW; FAA8BCEBAFC165AC CRC64;							
QY	Query Match	39.3%;	Score 707;	DB 11;	Length 159;			
QY	Best Local Similarity	88.1%;	Pred. No. 1.9e-50;					
QY	Matches 140;	Conservative 11;	Mismatches 8;	Indels 0;	Gaps 0			
QY	192 MOVVDFLSNNKODYKTEILSEKPLLIHTGMRCLTIDSVSLAMIDRIKRLKLSH							
Db	1 MOVIAFLSDPRLQYKTEILSEKPLLIHTGMRCLTIDSVSLAMIERIKRLKLSH							
QY	252 RIALGVGRLESQVKKVVALCAGSGSSVLOGVEADLYLTGEMSHHDPLDAAGCINVTLE							
Db	61 RIALGVGRLESQVKKVVALCAGSGSSVLOGVEADLYLTGEMSHHDVLAAGKINVTLE							
QY	312 HSNTERGFLSDRLMDSHLEKKINILSETRPDPLQVY 350							
Db	121 HSNTERGFLSELDQEMLGVEFENKINILSETRPDPLRV 159							

[illegible]

RC STRAIN-ATCC 12228;  
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,  
RA Chen Z., Men Y.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AE016748; AAC004845.1; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 366 AA; 41639 MW; BF73A88EE77462A1 CRC64;

Query Match 17.3%; Score 312; DB 16; Length 366;  
Best Local Similarity 24.9%; Pred. No. 2.3e-17;  
Matches 100; Conservative 80; Mismatches 130; Indels 92; Gaps 16;

QY 1 MDKALLSLNDPASFASMDNVGLVSPSPHTVTLTNDLDEEYMEVYLQKAD 60  
DB 1 MKISELMEVLNNHVPVPHQAESMDNVGLI-GNDKLDITGLITLTDCTDDVNNALNTN 59  
QY 61 LIISYHPPIPRPKRITMTWTKERLYRALENVGIYSPTAYDAAPQGVNNMLAGLGA 120  
DB 60 TIIAHHPILFKGVKRIYEDGYGS-IIRKLQNNINILALHTNDVNPQGVNMLADQIGL 118  
QY 121 CTSRPIHPSKAPRYPT-----EGNHRVEENV----- 147  
DB 119 ENISMINTNSYTYKQVTEIPKRYIEDFKDSLNEGLAEGNVEYCFESISKGQKRPVG 178  
QY 148 ---YTQDLKVASAVKIDGVSVTSFSAFTGNEQTRINLCTOKALMO-----VVD 196  
DB 179 DASPIYKGLD---SIEYDEIKL-EMIK-GNE-----LETKRIALDNHPEYTPVD 226  
QY 197 FLSRNKOLYQTEILSLERPLLHTGMGLCTLDESVSATMTDIRIKRLKLSHRLALG 256  
DB 227 FIKMKE-----SEYGLIGLQNLQMTLDEFSEYAKQKLNIPSVRY--- 268  
QY 257 VGRTEISOVKYVALCAGSGSVLQVE-----ADLYLGEASHHDITLDAAGQINVL 309  
DB 269 TGGH-DSPIKKVAIIIGSGSI---GEYKASQLGADVFEVYDGIKHHDALDKIQLNVL 323  
QY 310 CEHSNTERGFLSDRLMDLSHL---ENKNIITLSETDRDPLQ 348  
DB 324 INH-VSEYWKKEGLKELKELFKYENQPIYASEINTDPFK 364

RESULT 5  
ID O8EPZ0 PRELIMINARY; PRT; 372 AA.  
AC O8EPZ0;  
DT 01-MAR-2003 (TREMblrel. 23, Created)  
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
DE Hypothetical conserved protein.  
GN O81940.  
OS Oceanobacillus thelyensis.  
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.  
ON NCB1\_TaxID=182710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-HTE831 / DSM 14371 / JCM 11309;  
RX MEDLINE=2220767; PubMed=12235376;  
RA Takami H., Takaki Y., Uchiyama T.;  
RT "Genome sequence of Oceanobacillus thelyensis isolated from the Iheya  
RT Ridge and its unexpected adaptive capabilities to extreme  
RT environments.";  
RL Nucleic Acids Res. 30:3927-3935(2002).  
DR EMBL: AP004599; BAC13896.1; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 372 AA; 41869 MW; B66B9C95C8749C43 CRC64;

Query Match 17.2%; Score 309.5; DB 16; Length 372;  
Best Local Similarity 28.1%; Pred. No. 3.8e-17;  
Matches 105; Conservative 70; Mismatches 152; Indels 47; Gaps 13;

QY 9 SLNDFSLSPAESMDNVGLVSPSPHTVTLTNDLDEEYMEVYLQKADLILSYHP 68  
DB 14 AMDVAPKHLAYDMDNVGLQIGSFNATSKVL-ITLDVETESVYVDEALEKMNILIAHSL 72

QY 69 IFRPKRITWTKERLYRALENVGIYSPTAYDAAPQGVNNMLAKGLACTSRPIHP 128  
DB 73 LFQPLKQINNDITKGRVQKLIKNDIYVASHNLDAANNQVMDMLATELKLHTTTP-- 130  
QY 129 SKAPNPTTEGNHVEENVNTOD-LDKVASAVKIDGVSVTSFSART----- 174  
DB 131 --VPVY-NEKNRYV---YIVPESHIEKINQAFAESGAGYIGNVSHOTFSPGQGTFFPL 184  
QY 175 -----GNE-----EQTINLNCOKALMOY-DELSRNKOLYQTEILSLERPLLLH 220  
DB 185 EGTDPYIGEDQKITTYVDEYKIEITYVESILSNVKSILSAHPYEPAYDIYPLENK-TTN 243  
QY 221 TGMGRCTLDESVALTMDIRIKRLKLSHRLALGVGRLESQVKVALCAGSGSVLQ 280  
DB 244 FGIGRIGNLTPPTLDSFITYKTOFQLEBIR---ISGNKDKIKRVALIGSGSEKYVS 299  
QY 281 GV---EADLYLGEASHHDITLDAAGQINVLCEHSNTERGFLSDRLMDLSHL-NKIN 336  
DB 300 HAMRKADVYITGDMFPHIQDAAEMGLTYIDAGH-YIEKVMYTYTKQLAQTMELDKDF 358  
QY 337 IILSETDRDPLQYV 350  
DB 359 IEVSEINTDPFOFY 372

RESULT 6  
ID O8NM89 PRELIMINARY; PRT; 366 AA.  
AC O8NM89;  
DT 01-OCT-2002 (TREMblrel. 22, Created)  
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
DE Hypothetical protein MM1511.  
GN MM1511.  
OS Staphylococcus aureus (strain MM2).  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
ON NCB1\_TaxID=196620;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22040717; PubMed=12044378;  
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,  
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,  
RA Yamamoto K., Hiramatsu K.;  
RT "Genome and virulence determinants of high virulence community-  
RT acquired MRSA.";  
RL Lancet 359:1819-1827(2002).  
DR EMBL: AP004827; BAB95376.1; -  
DR InterPro: IPR002678; DUF34.  
DR Pfam: PF01784; DUF34.1.  
DR TIGRFAMs: TIGR00486; TIGR00486.1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 366 AA; 41153 MW; FALF28762D878C79 CRC64;

Query Match 15.5%; Score 279; DB 16; Length 366;  
Best Local Similarity 25.9%; Pred. No. 1.2e-14;  
Matches 102; Conservative 69; Mismatches 151; Indels 72; Gaps 16;

QY 1 MDKALLSLNDPASFASMDNVGLVSPSPHTVTLTNDLDEEYMEVYLQKAD 60  
DB 1 MKIADLMTLLDHHVFPSTAESMDNVGLIDEDDEVYGVLTALDCTLEVVNNEAIEKYN 59  
QY 61 LIISYHPPIPRPKRITMTWTKERLYRAL-ENRVGIYSPTAYDAAPQGVNNMLAKGLG 119  
DB 60 TIIASHHPILFKGVKRIYEDGYGS-GLIRKLQHDINILAHNTNDVNPQGVNMLAKAWG 117  
QY 120 ACTSRPIHPSKAPRYPT-----EGNHRVEENV-----NVTYQDL 152  
DB 118 LKNISITNNQDYYIKKQVTEIPKDNVGFQDKLSENGLAEGNVEYCFESISKGQKRPV 177  
QY 153 DKVASAVKIDGVSVTSFSAFTGNEQTRINLCTOKALMOYVDFLSRNKOLYQK----- 207  
DB 178 GEANPTIGQIDKIEYV-----DEVKIEFMIDAYQK-----SRADQLIKOYHPYE 221





Db 6 VIQAYEAFCPQEFSEMGSDSGLOI-GTLDKGIQRYVWALDIRREYVAEATEKGVDLTIK 64  
QY 66 HPIIFRPKRIITWTKERLVIRALENRVCISYSPHTAYDAPOGVNMMKAGACTSRP 125  
Db 65 HAPIFRPKIDLASRPQNOIYIDLIKHDIAVYVSHNIDIVENGNDWFCOML----- 117  
QY 126 IHPKAPNTEYEGNHRREFVNVNTQDLDKMSAVKGDGVSYSFSARTGNEQOTRINLN 185  
Db 118 -----GIEETTYLOETGPER----- 132  
QY 186 CTOKALMQVVDFTLSRNKQLYKTEILSLERPLIHTGMGRCTLDESVSATMIDRIKRH 245  
Db 133 -----GIGRIGNI-QPQTFMELAQYKQY 155  
QY 246 LKISHIRLALGVGTLESQYKVAALCAGSSSVLQGV---EADLYLTGEMSHDITDAAS 302  
Db 156 FIDSLHMYHYQENDLQKPSIRVAICGSGSEFKDALAKAGADYITGDYIYHTAQMLLS 215  
QY 303 OGIVVILCEHSNTERGFLSDLRDLDSHLENK---INIISETDRDPLQ 348  
Db 216 DGLALDPGH-YIEVLFVERKIALLTQWKEKWELEILDSQASTNPF 263

## RESULT 12

08G5M5 PRELIMINARY; PRT; 309 AA.  
AC 08G5M5;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Conserved hypothetical protein with duf34.  
CN BL0984.  
OS Bifidobacterium longum.  
OC Bacteria; Actinobacteria; Actinobacteriales; Bifidobacteriales;  
OC Bifidobacteriaceae; Bifidobacterium.  
OX NCBI\_Taxid=216816;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NC 2705;  
RX MEDLINE=22294977; PubMed=12381787;  
RA Schell M.A., Karimiantzou M., Snel B., Vilanova D., Berger B.,  
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,  
RA Pridmore R.D., Arigoni F.;  
RT "The genome sequence of Bifidobacterium longum reflects its adaptation  
RT to the human gastrointestinal tract."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
DR EMBL; AE014721; AAN24792.1;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 309 AA; 33851 MW; 68344899059F0F03 CRC64;

Query Match 11.3%; Score 203.5; DB 16; Length 309;  
Best Local Similarity 21.8%; Pred. No. 1.6e-08;  
Matches 67; Conservative 45; Mismatches 106; Indels 89; Gaps 5;

QY 2 DLKALLSLNDFASLFAESMDNGLYSPRPHVTNLTFLNLTLEEMVEYLQKKDL 61  
Db 6 NLKQYIDVLETLFLYLRKAEEMDEPLIV-GDLSHDVHTIYVAADPTSAITDKAATGADL 64  
QY 62 ILSTHPIFRPKRIITWTKERLVIRALENRVCISYSPHTAYDAPOGVNMMKAGACT 121  
Db 65 LITHHPIFRFVHETSGIFRGDIYRLYHGCGGLWCHTNADAAYRGVGAADYFELI 124  
QY 122 TSRIHPKAPNTEYEGNHRREFVNVNTQDLDKMSAVKGDGVSYSFSARTGNEQOTR 181  
Db 125 DQKPLVPIIDAN---ASHPV----- 141  
QY 182 INLNCQKALMQVVDFTLSRNKQLYKTEILSLERPLIHTGMGRCTLDESVSATMIDR 241  
Db 142 -----GLGRVGRPLPKPVALKDFQR 161  
QY 242 IKRHLKISHIRLALGVGTLESQ--VKVVALCAGSSSVLQGV---DLYLTGEMSHD 296  
Db 162 VFDEVSDHGRTSALGIGVCGSDTFVQYVALIPSGSDSLFNEVRATGVADYVYTSRLRHP 221

QY 297 TLDASQ 303  
Db 222 VTDAIEQ 228

## RESULT 13

08DT99 PRELIMINARY; PRT; 262 AA.  
ID 08DT99;  
AC 08DT99;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Conserved hypothetical protein.  
CN SM0.1463C.  
OS Streptococcus mutans.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_Taxid=1309;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UA159 / ATCC 700610 / Serotype C;  
RX MEDLINE=22295063; PubMed=12397186;  
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,  
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Ian S., Qian Y.,  
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;  
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental  
RT pathogen."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).  
DR EMBL; AE014978; AAN59121.1;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 262 AA; 29740 MW; A5740C55B8E248B CRC64;

Query Match 10.5%; Score 189.5; DB 16; Length 262;  
Best Local Similarity 20.8%; Pred. No. 1.8e-07;  
Matches 66; Conservative 50; Mismatches 100; Indels 101; Gaps 10;

QY 37 VNTLEFLNDLLEEMVEYLQKKADLIISYHPFRPKRIITWTKERLVIRALENRVGI 96  
Db 36 IKRIMIALDVETTYVAEIEKRVLLIYKHAIPTRPLNLY-ETANQHHIIFNLKHDIAV 94  
QY 97 YSPHTAYDAPOGVNMMKAGACTSRPIHSPKAPNYPREGNHRVEFNWYTDLDKVM 156  
Db 95 YVSHNTNIDYVDGLDMFCDDLIDKNNRIISPMSD----- 129  
QY 157 SAVKGDGVSYSFSARTGNEQOTRINLCTOKALMQVVDFTLSRNKQLYKTEILSLER 216  
Db 130 -----DY----- 131  
QY 217 LLHTGMGRCTLDESVSATMIDRIKRHLKLSHRL-ALGVGTLESQYKVAALCAGSG 275  
Db 132 -----GIGRVGDI-SPUSFEDLAKVKKIFMLDSVRLVSGEENPLISR--VAICGSG 182  
QY 276 SSVLQGV---EADLYLTGEMSHDITDAASOGIVNVILCEHSNTERGFLSDLRMD--SH 330  
Db 183 OSFYGEALTKGAQYIYTGDIYHTAQEMLTNGLLALDPGH-HIVLFVRELAEKFGQTWSC 241  
QY 331 LEN-KINIISETDRP 346  
Db 242 QENNDITLIESQVNTNP 258

## RESULT 14

P95777 PRELIMINARY; PRT; 262 AA.  
AC P95777;  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE ORF4 protein.  
OS Streptococcus mutans.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.

OX NCBI\_TaxID:1309;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Xc;  
RX MEDLINE=97175539; PubMed=9023194;  
RA Tsukikake Y., Yamashita Y., Oho T., Nakano Y., Koga T.;  
RT "Biological function of the dTDP-thiamose synthase pathway in  
R Streptococcus mutans";  
RL J. Bacteriol. 179:1126-1134(1997).  
DR EMBL; D78182; BA011246.1; -;  
DR InterPro; IPR002678; DUF34.  
DR Pfam; PF01784; DUF34. 1.  
DR TIGRfams; TIGR00486; TIGR00486. 1.  
SQ SEQUENCE 262 AA; 29723 MW; 68E0DBB5A6002DE3 CRC64;

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